

1 GCGGCAGCGG CGGCGGCTGA GGAGGGCCCC GCCTGCGAGA GCCTCAGTGG
 51 GAGCCGGCTC AGCCCTCGGC CACCATGTCT GCGCCGTCGG AGGAGGAGGA
 101 GTACGCGCGG CTGGTGATGG AGGCGCAGCC GGAGTGGCTG CGCGCCGAGG
 151 TGAAGCGGCT GTCCACGAG CTGGCCGAGA CCACGCGTGA GAAGATCCAG
 201 GCGGCCGAGT ACGGGCTGGC GGTGCTCGAG GAGAAGCACC AGCTCAAGCT
 251 GCAGTTCGAG GAGCTCGAGG TGGACTATGA GGCTATCCGC AGCGAGATGG
 301 AGCAGCTCAA GGAGGCCTTT GGACAAGCAC ACACAAACCA CAAGAAGGTG
 351 GCTGCTGACG GAGAGAGCCG GGAGGAGAGC CTGATCCAGG AGTCGGCCTC
 401 CAAGGAGCAG TACTACGTGC GGAAGGTGCT AGAGCTGCAG ACGGAGCTGA
 451 AGCAGTTGCG CAATGTCTCT ACCAACACGC AGTCGGAGAA TGAGCGCCTG
 501 GCCTCTGTGG CCCAGGAGCT GAAGGAGATC AACCAGAATG TGGAGATCCA
 551 GCGTGGCCGC CTGCGGGATG ACATCAAGGA GTACAAATTC CGGGAAGCTC
 601 GTCTGCTGCA GGACTACTCG GAACTGGAGG AGGAGAACAT CAGCCTGCAG
 651 AAGCAAGTGT CTGTGCTCAG ACAGAACCAG GTGGAGTTTG AGGGCCTCAA
 701 GCATGAGATC AAGCGTCTGG AGGAGGAGAC CGAGTACCTC AACAGCCAGC
 751 TGGAGGATGC CATCCGCCTC AAGGAGATCT CAGAGCGGCA GCTGGAGGAG
 801 GCGCTGGAGA CCCTGAAGAC GGAGCGCGAA CAGAAGAACA GCCTGCGCAA
 851 GGAGCTGTCA CACTACATGA GCATCAATGA CTCCTTCTAC ACCAGCCACC
 901 TGCATGTCTC GCTGGATGGC CTCAAGTTCA GTGACGATGC TGCCGAGCCC
 951 AACAACGATG CCGAGGCCCT GGTCAATGGC TTTGAGCAGC GCGGCCTGGC
 1001 CAAGCTGCCA CTGGACAACA AGACCTCCAC GCCCAAGAAG GAGGGCCTCG
 1051 CACCGCCCTC CCCAGCCTC GTCTCCGACC TACTCAGTGA GCTCAACATC
 1101 TCTGAGATCC AGAAGCTGAA GCAGCAGCTG ATGCAGATGG AGCGGGA AAA
 1151 GGCGGGCCTG CTGGCAACGC TGCAGGACAC ACAGAAGCAG CTGGAGCACA
 1201 CGCGGGGCTC CCTGTCAGAA CAGCAGGAGA AGGTGACCCG CCTCACAGAG
 1251 AATCTGAGTG CCCTGCGGCG CCTGCAGGCC AGCAAGGAGC GGCAGACAGC
 1301 CCTGGACAAC GAGAAGGACC GTGACAGCCA TGAGGATGGG GACTACTACG
 1351 AGGTGGACAT CAACGGGCCT GAGATCTTGG CCTGCAAGTA CCATGTGGCT
 1401 GTGGCTGAGG CTGGCGAGCT CCGCGAGCAG CTCAAGGCAC TGCGCAGCAC
 1451 GCACGAGGCT CGTGAGGCC AGCACGCCGA GGAGAAGGGC CGCTATGAGG
 1501 CTGAGGGCCA GGCACCTACG GAGAAGGTCT CCCTGCTAGA GAAGGCCAGC

FIGURE 1

1551	CGCCAGGACC	GCGAGCTGCT	GGCCCCGGCTG	GAGAAGGAGC	TAAAGAAGGT
1601	GAGCGACGTC	GCCGGCGAGA	CACAGGGCAG	CCTGAGTGTG	GCCCAGGATG
1651	AGCTGGTGAC	CTTCAGTGAG	GAGCTGGCCA	ATCTCTACCA	CCACGTGTGC
1701	ATGTGCAACA	ATGAGACACC	CAACCGTGTC	ATGCTGGACT	ACTACCGCGA
1751	GGGCCAGGGC	GGGGCCGGCC	GCACCAGTCC	CGGGGGCCGC	ACCAGCCCCG
1801	AGGCGCGTGG	CCGGCGCTCA	CCCATCCTCC	TACCCAAGGG	GCTGCTGGCT
1851	CCTGAGGCGG	GCCGAGCAGA	TGGTGGGACG	GGGGACAGCA	GGCCCTCGCC
1901	TGGCTCCTCA	CTGCCATCAC	CCCTGAGTGA	CCCACGCCGG	GAGCCCATGA
1951	ACATCTACAA	CCTGATCGCT	ATCATCCGTG	ACCAGATCAA	GCACCTGCAG
2001	GCAGCCGTGG	ACCGCACCAC	GGAGCTGTCA	CGCCAGCGCA	TTGCTCTCTA
2051	GGAGCTGGGC	CCCGCCGTGG	ACAAGGACAA	GGAAGCGCTT	ATGGAGGAGA
2101	TCCTCAAGCT	GAAGTCGCTG	CTCAGCACCA	AGCGGGAGCA	GATCACCACG
2151	CTGCGCACTG	TGCTCAAGGC	CAACAAGCAG	ACGGCCGAGG	TGGCCCTTGC
2201	CAACCTGAAG	AGCAAGTATG	AGAATGAGAA	GGCCATGGTT	ACCGAGACCA
2251	TGATGAAGCT	GCGCAATGAG	CTCAAGGCCC	TCAAGGAGGA	CGCAGCCACC
2301	TTCTCCTCGC	TGCGTGCTAT	GTTTGCCACC	AGGTGTGACG	AGTACATTAC
2351	ACAGCTGGAT	GAGATGCAGC	GGCAGCTGGC	GGCTGCTGAG	GACGAGAAGA
2401	AGACGCTGAA	CTCGCTGCTG	CGCATGGCCA	TCCAGCAGAA	GCTGGCGCTG
2451	ACCCAGCGGC	TGGAGCTGCT	CGAGCTGGAC	CATGAGCAGA	CCCGGCGTGG
2501	CCGTGCCAAA	GCCGCCCCGA	AGACCAAGCC	AGCCACACCG	AGCCTGTAGA
2551	GTAGCTGCCA	GGAGGACTTG	GCCACCCGGC	CCTGTACAC	TGCAGCCCCT
2601	TCCCCTTCCC	TCTCGTGGCC	CACAAGGAGG	AAGGAAGGGC	AACCTAAAAG
2651	CCCACTTAGA	AACTTTTTGG	ATATGCCACT	GCAATTCTTT	TCAAAATAGC
2701	ATTCCCCAGG	TTTTTAATGG	GAGGAAAAAA	AGCTTTAATG	TTGAGCATGC
2751	TGCGAGCTGC	TGCGTGGAAG	GGCCTCTGTA	TGGGCCGAAG	ACCCTTCTTC
2801	CCTGGCTGCC	AGGCTCGCCA	GGAGCCCACT	GGAAACGCCC	ACCACGGGGG
2851	CTCCTTGTTA	CACATGTTCT	TTTTTTATCC	GATCAACCTG	TGCACTTTTG
2901	ATATTTTGAT	ATTATATTTG	CTTCCTTAAT	TCCTCGCGTA	GAGACGGTCT
2951	CAGGTGCCGT	GGTCTATGCT	CGTGGTCCTG	TAGCTGTCCG	CCTCAGCTCC
3001	CACCGTGTTT	GTCTGGGTGC	AGCACGAGGC	AGAGCTGTGT	GCTCEATAGC
3051	GTGTAGCTTT	AGACTCGGAG	ATGAGTGCTT	TGACCCAGCG	AGGAGCTCAG
3101	CTAAGTGTAT	CCACGCTGTG	GTTTCAGCAGC	CTTTAGATCA	TACGGCATTG
3151	TGGTTCATGT	TTGAAAATTAC	AGATTTTAAA	TGCCATGTTT	ATTAAGAAAT

3201 CCAGGGTATT CAGATTCTGG GGTTTTTCAT ATTGTATTAT TATTATTCTT
3251 AGGAATAGTT CAATGTAACA AGAAGAAAAC TTGACCTTTG CTCTGGTTAA
3301 AACAGTAATA GGCACCTGAA AAAAAAAGAT AAATTATTGA ATGAGTAGTA
3351 TTACCTACAA ATTCCAGAAT TTTCTGGGTT TTAGGACGTT GTGAAGCATG
3401 ACTGATTAAAC AGAATTTTAT ACAACTGTAC CAATAAAATT CCAAATTGGA
3451 ATTGTTTTGT TACTCTGGTT GTTGTGCCAA ATTGTGGTAC ACTTAGAAAA
3501 TTCTACAGTC GTCGATTTTT AGGGTGTTCT CTTTCAACAC CTTTTTGTTA
3551 GTAATCATTG CCAGTAGTGC CTTCATCAGT TAAGGGAGGT GTCCCAGCAC
3601 AGATCATTCT CAAAAGCGAG CAGGGAAGAG CTAGTGGGCA TGCTGAAGGC
3651 CAGCGTGGAC AGCAGGTGAG GCAGGTGCTC CTCACACCCA GACCTGGGCA
3701 TCTTCATTGA GGGAAAGAAA ACAGTCATTG TGCAAAATTC TGTTAGTCAG
3751 TGATTCTTTA CTGCAAATT CAGGGGCTTA GAAAATGAAA GCAAACACAA
3801 AACCTTGAGT GTGCTTTGGG AACCAAATGG ACCTTCTGGG ACAAGCTGAG
3851 CAAGCTGTAT GAACGCCACG TTTGTGAAGA GCTGAGGGTA TCAGGAGGGC
3901 CGACGCTGTG TTGGCATGCG CAGTAGGGGA TGAGGGTTAG CCATAGTATT
3951 CTTTGCAAAT GTGAAAGCGA GACATTATAT CTTCTCTTGC TTGGTGTAAC
4001 TAATCACTGT TAATTTTCAGG AAACAGAACT CATTAAACT CCTTAGCAAA
4051 CCAGGTCTAC ATCCTGTTTT GTTTGCTGAG TGAGGTAGT GGGAGTGCTC
4101 AAATTGGTAC TCTTGAGGGA AGAAAACTG TCCTTCCTTC TCCAAAAAAG
4151 GAAAAATTAT AATAATATAA ATGACAAAAA TAAAAGAATT CTGTTTCCTG
4201 GAATAAGCAT TTCTTATTC TAGTTGTAGG GACTCCTATT TTTACCTTCC
4251 GTTACAGTGT TGATTCATAA GAAATATTGT TACATTTGAG ATAACCTCAT
4301 CTGTATGGGG TATTTATTTG CAATGATGTC TGAGTACTGT ATTTTTTCTG
4351 TGCATTACCT TAGTGTGAGA ATGTTGGTCT TTATTTTAAA GTCATATGCA
4401 TGTTCTCCTG CCAAGGAACC TTTACACAGA CCCAAACAAA AAAATAATAA
4451 TCAAATGCCT TCAATTTCTG AGAAAATGAG GCAGAGCATG GAAAAGGAAT
4501 AGGAAGGAGA AATTAATTGA GATTTTCAGG ACACAGACAT ATGATGTGAA
4551 TGCCTACAAA GCCAGTGTGC ATAGGAACAG TGGGCCTGGG TAAAGAGTCA
4601 CATTGGTAGG

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T08T90 T00T8860

1 MSAPSEEEY ARLVMEAQPE WLRAEVKRLS HELAETTREK IQAAEYGLAV
 51 LEEKHQKLQ FEELEVDYEA IRSEMEQLKE AFGQAHINHK KVAADGESRE
 101 ESLIQESASK EQYYVRKVLE LQTELKQLRN VLTINTQSENE RLASVAQELK
 151 EINQVETQR GRLRDDIKEY KFREARLLQD YSELEENIS LQKQSVLRQ
 201 NQVEFGLKH EIKRLEEETE YLNSQLEDAI RLKELSERQL EEALETLKTE
 251 REQNSLRKE LSHYMSINDS FYTSHLHVS L DGLKFSDDAA EPNDAAEALV
 301 NGFEHGLAK LPLDNKTSTP KKEGLAPPSP SLVSDLLSEL NLSETQKLKQ
 351 QLMQMERKA GLLATLQDTQ KQLEHTRGSL SEQQEKVIRL TENLSALRRL
 401 QASKERQ TAL DNEKDRDSHE DGDYYEVDIN GPEILACKYH VAVAEAGELR
 451 EQLKALRSTH EAREAQHAE E KGRYEAEQQA LTEKVSULEK ASRQDRELLA
 501 RLEKELKKVS DVAGETQGSL SVAQDELVTF SEELANLYHH VMCNNETPN
 551 RVMLDYYREG QQGAGRTSPG GRTSPEARGR RSPILLPKGL LAPEAGRADG
 601 GTGDSSPSPG SSLPSPLSDP RREPMTYNL IATIRDQIKH LQAAVDRITE
 651 LSRQRIASQE LGPAVDKIKE ALMEEILK LK SLLSTKREQT TILRTVLKAN
 701 KQTAEVALAN LKSKYENKA MVTEDMKLR NELKALKEDA ATFSSLRAMF
 751 ATRCDEYTTQ LDEMQRQLAA AEDEKKTINS LLRMAIQQKL ALTQRLELLE
 801 LDHEQTRGR AKAAPKTKPA TPSL*

FIGURE 2

1 ATGTGGGTGC TGGGOGAGTA OGAGOGACAC TGGGATTOCA TCAACTOGGA
 51 CTTTGGGAGC GAGTGOOGGG GTTGGGGGA CTOGAGTOG GGGGCTAGCG
 101 CCAGTCAGG GOGGOGAGOC GGGGGGGG OGGGGAGCA GGAGGAAGTG
 151 CACTACATOC CCATCOGGT OCTGGGOGC GGGGCTTUG GGAAGOCAC
 201 GCTGTACOGC OGCAOGAGG ATGACTCACT GGTGTGTGG AAGGAAGTGG
 251 ATTTGACOGC GCTGTCTGAG AAGGAAGTGC GTGATGCTT GAATGAGATT
 301 GTTATTCTGG CACTGCTGCA GCATGACAAC ATTATTGCT ACTACAATCA
 351 CTTTATGGAC AATAACAGC TGCTGATTGA GCTGGAATAT TGTAATGGAG
 401 GGAACCTGTA TGACAAAATC CTTGCTCAGA AGGACAAGTT GTTTGAGGAA
 451 GAGATGGTGG TGTGGTACCT ATTTCAGATT GTTTCAGCAG TGAGCTGCAT
 501 CCATAAAGCT GGAATCCTTC ATAGAGATAT AAAGACATTA AATATTTTTC
 551 TGACCAAGGC AAACTGATA AAACCTGGAG ATTATGGCT AGCAAAGAAA
 601 CTTAATTCTG AGTATTCCAT GGCTGAGAG CTTGTGGGA CCCCATTATTA
 651 CATGTCTOCA GAGCTCTGTC AAGGAGTAAA GTACAATTTC AAGTCTGATA
 701 TCTGGGCAGT TGGCTGOGTC ATTTTGAAC TGCTTACCT AAAGAGGAG
 751 TTTGATGCTA CAAACCCACT TAACTGTGT GTGAAGATG TGCAAGGAAT
 801 TGGGGCCATG GAAGTTGACT CTAGOCAGTA CTCTTTGGAA TTGATOCAAA
 851 TGGFTCATTC GTGCTTGAC CAGGATCTG AGCAGAGAC TACTGCAGAT
 901 GAACTTCTAG ATGGGCTCT TCTCAGGAAA CGCAGGAGAG AGATGGAGGA
 951 AAAAGTCACT CTGCTTAATG CACCTACAAA GAGAOCAAGG TCAAGCACTG
 1001 TGAAGTCAAGC AOCCTTGCT GTAGTAACAT CAGGAACAG TGAAGTCTAT
 1051 GTTTGGGGTG GTGGAAAATC CACCCCCAG AACTGGATG TTATCAAGAG
 1101 TGGCTGTAGT GGGGGCAGG TCTGTGAGG GAATACCCAC TTGCTGTGG
 1151 TCACAGTGA GAAGGAAGTG TACACTTGGG TGAACATGA AGGAGGCACT
 1201 AACTOCATG GTCAGCTGGG CCATGGAGAC AAAGCTCTT ATGACAGOC

FIGURE 3

1251 AAAGCATGTG GAAAAGTTGC AAGGCAAAGC TATCCATCAG GTGTCATGTG
1301 GTGATGATTT CACTGTCTGT GTGACTGATG AGGGTCAGCT CTATGCOCTTC
1351 GGATCAGATT ATTATGGCTG CATGGGGGTG GACAAAGTTG CTGGOOCTGA
1401 AGTGCTAGAA CCCATGCAGC TGAAC TTC TT CCTCAGCAAT CCAGTGGAGC
1451 AGGTCTOCTG TGGAGATAAT CATGTGGTGG TTCTGACAG AAACAAGGAA
1501 GTCTATTCTT GGGCTGTGG CGAATATGGA CGACTGGGTT TGGATTGAGA
1551 AGAGGATTAT TATACAOCAC AAAAGGTGGA TGTTCOAAG GCTTGATTA
1601 TTGTTGCAGT TCAATGTGGC TGTGATGGGA CATTTCGTG GACCCAGTCA
1651 GGCAAAGTGC TGGCTGTGG ACTCAATGAA TTCAATAAGC TGGGTCTGAA
1701 TCAGTGCATG TGGGAATTA TCAACCATGA AGCATACCAT GAAGTTCOCT
1751 ACACAAAGTC CTTTACCTTG GOCAAACAGT TGTCTTTTA TAAGATCOGT
1801 ACCATTGOC CAGGCAAGAC TCACACAGCT GCTATTGATG AGCGAGGCG
1851 GCTGCTGAC TTTGGCTGCA ACAAGTGTGG GCAGCTGGGC GTTGGGAAGT
1901 ACAAGAAGCG TCTGGGAATC AACCTGTGG GGGGACCOCT TGGTGGGAAG
1951 CAAGTGATCA GGGTCTOCTG CGGTGATGAG TTTACCATG CTGCCACTGA
2001 TGATAATCAC ATTTTTCOCT GGGGCAATGG TGGTAATGGC CGOCTGGCAA
2051 TGACOOCCAC AGAGAGACA CATGGCTCTG ATATCTGTAC CTCATGGOCT
2101 CGGCTATTT TTGGATCTCT GCATCATGTC CCGGACCTGT CTTCOOGTG
2151 ATGGCATAOC ATTCTCATOG TTGAGAAAGT ATTGAATTCT AAGACCATOC
2201 GTTCCAATAG CAGTGGCTTA TCATTGGAA CTGTGTTTCA GAGCTCTAGC
2251 CCGGAGAGG GGGGGGGGG CGGGGTGGT GAAGAAGAG ACAGTCAGCA
2301 GGAATCTGAA ACTOCTGAC CAAGTGGAGG CTTCOGAGA ACAATGGAG
2351 CAGACOGAG AATGGAAGGT TTAATCAGTC CCACAGAGC CATGGGGAAC
2401 AGTAATGGGG CCAGCAGCTC CTGTCTGGC TGGCTTGAAG AGGAGCTGGA
2451 AAATGCAGAA TTTATOOCCA TGCTGACAG CCAATCTOCT CTCAGTGCAG
2501 CGTTTTTCA ATCTGAGAAA GATAOCTGC CCTATGAGA GCTGCAAGGA

2551 CTCAAAGTGG CCTCTGAAGC TOCTTTGGAA CACAAACCC AAGTAGAAGC
2601 CTGTCACCT CGGCTGAATC CTGCAGTAAC CTGTGCTGGG AAGGGAACAC
2651 CACTGACTOC TOCTGGGTGT GGGTGCAGCT CTCTGCAGGT GGAGGTTGAG
2701 AGATTGCAGG GTCTGGTGTT AAAGTGTCTG GCTGAACAAC AGAAGCTACA
2751 GCAAGAAAAC CTCCAGATTT TTACCCAACT GCAGAAGTTG AACAGAAAT
2801 TAGAAGGAGG GCAGCAGGTG GGGATGCATT CCAAAGGAAC TCAGACAGCA
2851 AAGGAAGAGA TGGAAATGGA TOCAAAGCCT GACTTAGATT CAGATTCTCTG
2901 GTGCTCTCTG GGAACAGACT CCTGTAGACC CAGCCTCTAG

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1 MSVLGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
 51 HYIPIRVLGR GAFGEATLYR RTEDDSLTVW KEVDLTRLSE KERRDALNEI
 101 VILALLQHDN IIAYYNHFMD NTTLLIELEY CNGGNLYDKI LRQKDKLFEE
 151 EMVVWYLFQI VSAVSCIHKA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
 201 LNSEYSMAET LVGTPPYMSP ELCQGVKYNF KSDIWA VGC V IFELLTLKRT
 251 FDATNPLNLC VKIVQGIRAM EVDSSQYSLE LIQMVHSCLD QDPEQRPTAD
 301 ELLDRPLL RK RRREMEEKVT LLNAPTKRPR SSTVTEAPIA VVTSRTSEVY
 351 VWGGGKSTPQ KLDVIKSGCS ARQVCAGNTH FAVVTVEKEL YTWVNMQGGT
 401 KLHGQLGHGD KASYRQPKHV EKLQ GKAIHQ VSCGDDFTVC VTDEGQLYAF
 451 GSDYYGCMGV DKVAGPEVLE PMQLNFFLSN PVEQVSCGDN HVVVLTRNKE
 501 VYSWGCGEYG RLGLDSEEDY YTPQKVDVPK ALIIVAVQCG CDGTFLLTQS
 551 GKVLACGLNE FNKLGLNQCM SGIINHEAYH EVPN TTSFTL AKQLSFYKIR
 601 TIAPGKTHTA AIDERGRLLT FGCNKCGQLG VGNYKKRLGI NLLGGPLGGK
 651 QVIRVSCGDE FTIAATDDNH IFAWGNGGNG RLAMTPTERP HGSDICTSWP
 701 RPIFGSLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSGL SIGTVFQSSS
 751 PGGGGGGGGG EEEDSQQESE TPDPSGGFRG TMEADRGMEG LISPTEAMGN
 801 SNGASSSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPYEELQG
 851 LKVASEAPLE HKPQVEASSP RLNPAVTCAG KGTPLTPPAC ACSSLQVEVE
 901 RLQGLVLKCL AEQQKLQQEN LQIFTQLQKL NKKLEGGQQV GMHSGKTQTA
 951 KEEMEMDPKP DLDSDSWCLL GTDSCRPSL*

FIGURE 4

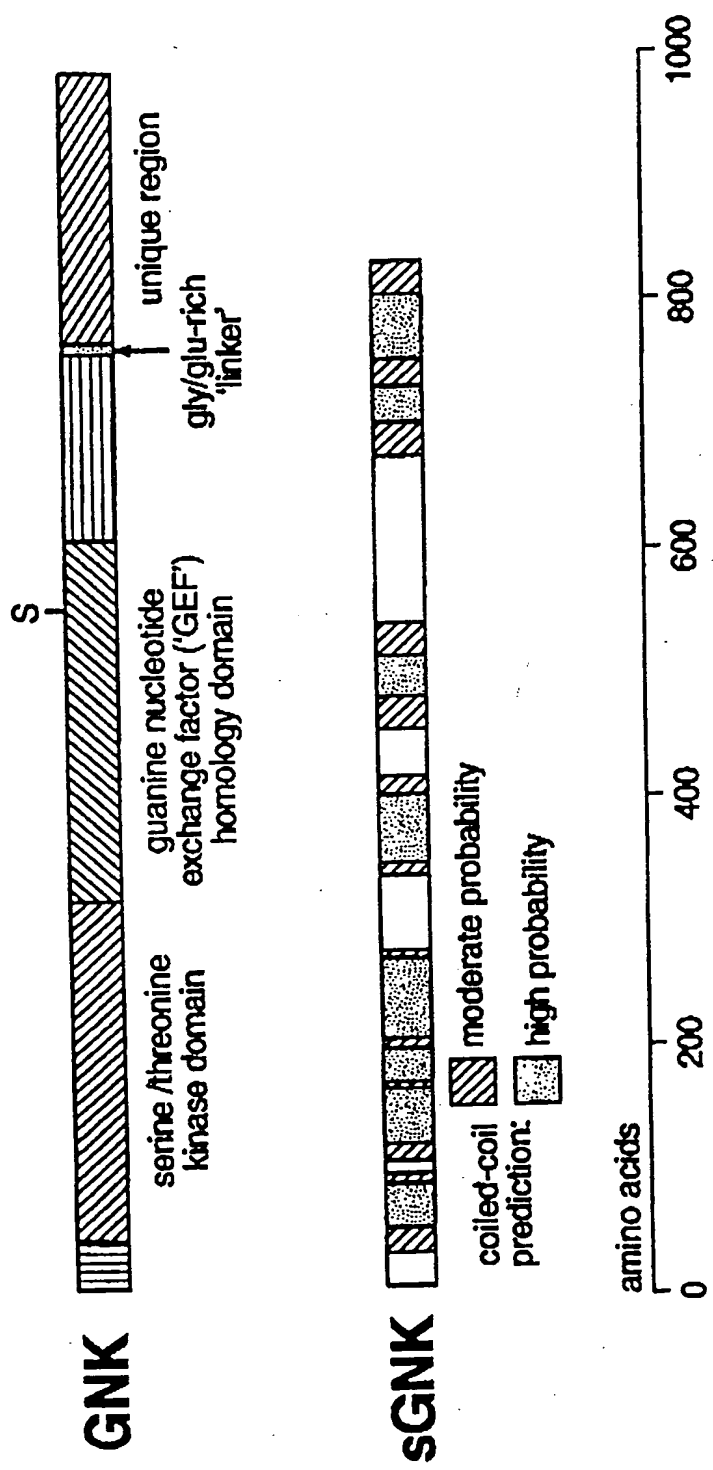


FIGURE 5

Putative GNK Domains and Structural Features

KINASE (44-315)

GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) (318-605)

GLYCINE/ACIDIC-RICH TETHER (752-764)

C-TERMINAL DOMAIN WITH NO KNOWN HOMOLOGY OR FUNCTION (765-979)

1 MSVLGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
 51 HYIPIRVLGR GAFGEATLYR RTEDDSLTVVW KEVDLTRLSE KERRDALNEI
 101 VILALLQHDN IIAYYNHFMD NTTLLIELEY CNGGNLYDKI LRQKDKLFEE
 151 EMVVWYLFQI VSAVSCIHA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
 201 LNSEYSMAET LVGTPPYMSP ELCQGVKYNF KSDIWA VGC V IFELLTLKRT
 251 FDATNPLNLC VKIVQGIRAM EVDSSQYSLE LIQMVHSCLD QDPEQRPTAD
 301 ELLDRPLL RK RRREMEEKVT LLNAPTKRPR SSTVTEAPIA VVTSRTSEVY
 351 VWGGGKSTPO KLDVIKSGCS AROVCAGNTH FAVVTVEKEL YTWVNMOGGT
 401 KLHGOLGHGD KASYROPKHV EKLOGKAIHQ VSCGDDFTVC VTDEGQLYAF
 451 GSDYYGCMGV DKVAGPEVLE PMOLNFFLSN PVEQVSCGDN HVVVLTRNKE
 501 VYSWGCGEYG RLGLDSEEDY YTPQKVDVPK ALIIVAVOCG CDGTFLLTOS
 551 GKVLACGLNE FNKLGLNOCM SGIINHEAYH EVPNYSFTL AKQLSFYKIR
 601 TIAPGKTHTA AIDERGRLLT FGCNKGQLG VGNYKKRLGI NLLGGPLGGK
 651 QVIRVSCGDE FTIAATDDNH IFAWGNGGNG RLAMTPTERP HGSDICTSWP
 701 RPIFGSLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSGL SIGTVFQSSS
 751 PGGGGGGGGG EEEDSQQESE TPDPSGGFRG TMEADRGMEG LISPTTEAMGN
 801 SNGASSSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPYEELQG
 851 LKVASEAPLE HKPQVEASSP RLNPVAVTCAG KGTPPLTPAC ACSSLQVEVE
 901 RLOGLVLKCL AEQOKLOQEN LOIFTLOKL NKKLEGGQOV GMHSGKTOTA
 951 KEEMEMDPKP DLDSDSWCLL GTDSCRPSL

FIGURE 6

Bicaudal D -----MAAEEVLQTVDHY
 sGNK -----MSAPSEEEYARLVMEAQPEWL
 C-NAP1 (aa 121) NTHLEAQLQKAAEAGAEQLADLRDIQEEKEEIQKKLSERHQQAATTQLEQLHQEAKKQ

Bicaudal D KTEIERLTKELTETTHEKIQAAEYGLVVLEEKLTCLKQYDELEAEYDSLKQELEQLKEAF
 sGNK RAEVKRLSHELAEETREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEAIRSEMEQLKEAF
 C-NAP1 EEVLARAVQKEKEALVREKAALEVRLQAVERDRQDLAEQLQGLSSAKELLESSLFEAQQQN

Bicaudal D GQSFSIHRKVAEDGETREETLLQESASKEAYYLGKILEMQNELKQSRVVTVNQAENERL
 sGNK GQAHTNHKKVAADGESREESLIQESASKEQYVVRKVLELQTELKQLRNVLTNTQSENERL
 C-NAP1 SVIEVTKGQLEVQIQTVTQAKEVIQGEVRCCLKLELDTERSQAE-QERDAAARQLAQAEQE

Bicaudal D TAVVQDLKENNEMVELQRIKMKDEIREYKFRERLLQDYTELEENITLQKLVTSLKQNKQ
 sGNK ASVAQELKEINQNVIEIQGRRLRDDIKEYKFRERLLQDYSELEENISLQKQVSVLRNQ
 C-NAP1 GKTALEQQKAAHEKEVNQLREKWE-KERSWHQQLAKALESLEREKMELEMLRKEQ-QTE

Bicaudal D VEYEGLKHEIKRFEETVLLNSQLEDAIRLKEIAEHQLEEALETCLKNEREQKNNLRKELS
 sGNK VEFEGLKHEIKRLEETVLLNSQLEDAIRLKEISERQLEEALETCLKTEREQKNSLRKELS
 C-NAP1 MEAIQAQREERTQAESALCQMQLTEKERVSLLETLLQTQKELADASQQLERLRQDMKV

Bicaudal D QYISLND---NHISISVDGLKFAEDGSEPN--DDKMNGHIHGPLVKLNGDYRTPTLRK
 sGNK HYMSINDSFYTSHLHVSLLDGLKFSDDAAEPNNDAAELVNGFEHGGGLAKLPLDNKTSTPKK
 C-NAP1 QKLKEQETTGILOTQLQEAQRELKEAARQHRDDLALQEESSSLQDKMDLQKQVEDLKS

Bicaudal D ----GESLNPVSDLFSELNISEIQKLKQQLMQVEREKAILLANLQESQTQLEHTKGALTE
 sGNK EGLAPPSPLVSDLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRGSLSE
 C-NAP1 QLVAQDDSQRLVEQEVQEKLRQTEYNRIQKELEREKASLTLSLMEKEQRLLLVLQEADSI

Bicaudal D QHERVHRLTEHVNAMRGLQSSKELKAELDGEKGRDSGEEAHDYVDINGLEILECKYRVA
 sGNK QQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDGDYVEVDINGPEILACKYHVA
 C-NAP1 RQQLSALRQDMQEAQGEQKELSAQMELLRQEVKEK-EADFLAQEAQLLEELEASHITEQ

Bicaudal D VTEVIDLKAIEIKALKEKYNKSVENYTDKAKYESKIQMYDEQVTSLEKTTKESGEKMAHM
 sGNK VAEAGELREQLKALRSTHEAREAQHAEEKGRYEAEGQALTEKVSLLKASRQDRELLARL
 C-NAP1 QLRLSLWAQEAQAAQLQLRLRSTESQLEALAAEQPGNQAQAQALASLYSALQALGSV

Bicaudal D EKELQKMTSIANENHSTLNTAQDELVTFSSELAQLYHHVCLNNETPNRVMLDYRQSRV
 sGNK EKELKKVSDVAGETQGSLSVAQDELVTFSSELANLYHHVCMNNETPNRVMLDYRREG--
 C-NAP1 CESRPFLSGGDSAPSVMGLEPDQNG--ARSLFKRGPLLTALSAEAVASALHKLHQDLWK

Bicaudal D TRSGSLKGPDDPRGLLSPRLARRGVSSPVETRTSSEPVAKESTEPSKEPSPTKTPTISPV
 sGNK -QGG--AGRTSPGGRTSP--EARGRRSPILL-----PKGLLAPEAGRADGGTGDSSPSPG
 C-NAP1 TQQTRDVLRDQVQKLEERLTDTEAKESQVHTELQDLQRQLSQNQEEKSKWEGKQNSLESE

Bicaudal D ITAPPSPVLDTSDIRKEPMNIYNLNAIIRDQIKHLQKAVDRSLQLSRQRAARELAPMI
 sGNK SSLP--SPLSDP--RR-EPMNIYNLIAIIRDQIKHLQAAVDRTTELSRQRIASQELGPAV
 C-NAP1 LMELHETMASLQSRRLRRAELQRMQAQGER----ELLQAAKENLTAQVEHLQAAVVEARAQ

Bicaudal D DKDKKEALMEEILKLKSLSTKREQIATLRAVLKANKQTAEVALANLKNKYENEKAMVTET
 sGNK DKDKKEALMEEILKLKSLSTKREQITTLRTVLKANKQTAEVALANLKNKYENEKAMVTET
 C-NAP1 ASAAGILEEDLRTARSALKLNKEEVESERERAAQALQEQGELKVAQGKALQEN-LALLTQT

Bicaudal D MTKLRNELKALKEDAAATFSSLRTMFATRCDEYVTQLDEMQRQLAAAEDEKKTLLNTLLRMA
 sGNK MMKLRLNELKALKEDAAATFSSLRTMFATRCDEYITQLDEMQRQLAAAEDEKKTLLNSLLRMA
 C-NAP1 LAEREEVEVETLRGQIQELEKQREMKALELLSLDLKRNQEVVDLQEQIQELEKCRSVL

Bicaudal D IQQKLALTQRLLEDLEFDHEQSRSSKGLG-KSKIGSPKV (-> 154 aa)
 sGNK IQQKLALTQRLLELDHEQTRRGRKAAPKTKPATPSL*-----
 C-NAP1 EHLPMAVQEREQKLTQVQREQIRELEKDRETQRNVLEHQL (-> 914 aa)

Comparison of sGNK with coiled-coil domains of Human Bicaudal D and the human centrosomal NEK-1 substrate protein C-Nap1

FIGURE 7

sGNK is a substrate for GNK *in vitro*.

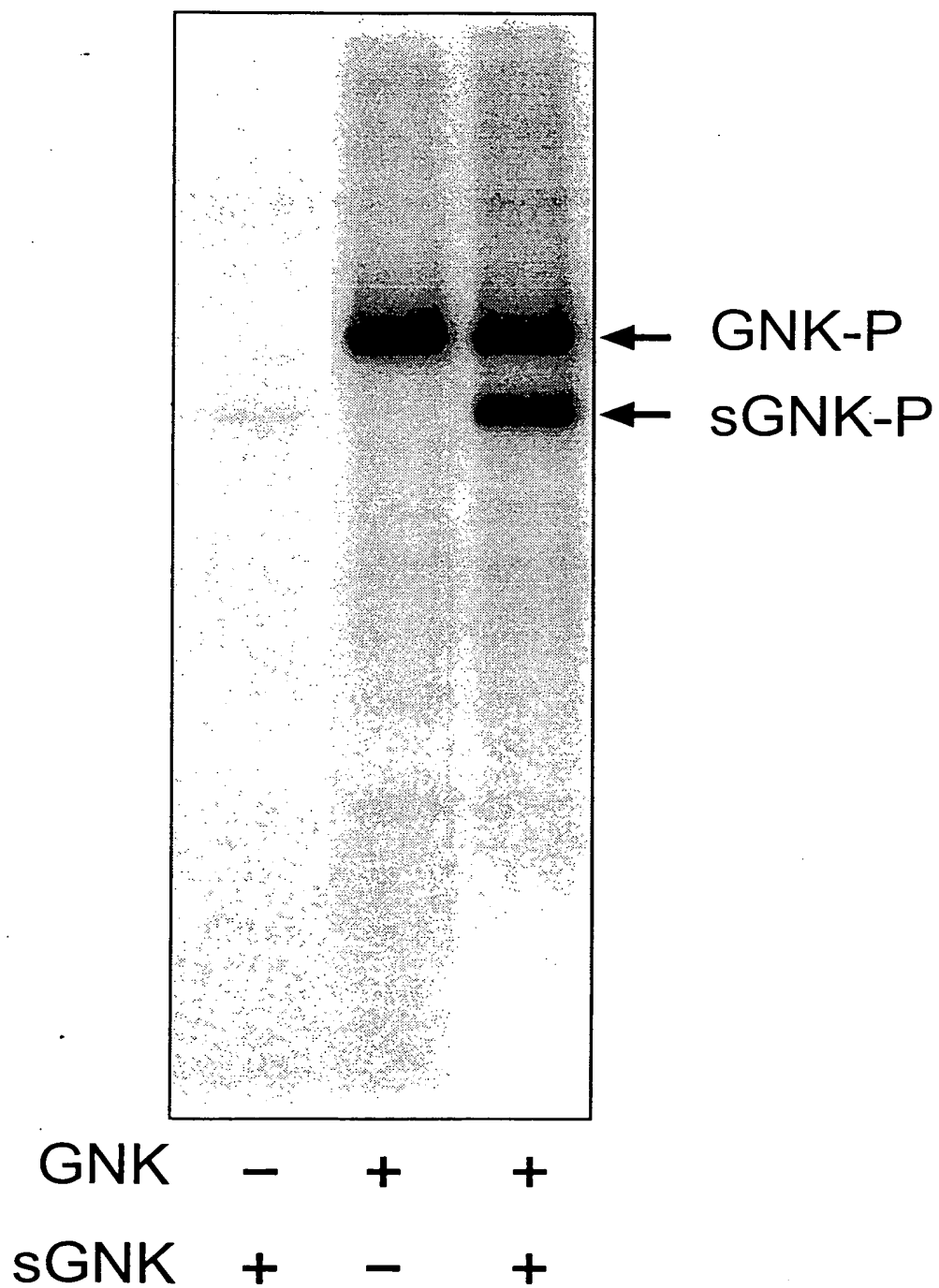


FIGURE 8

**Final GNK purification step:
microbore Mono Q column chromatography**

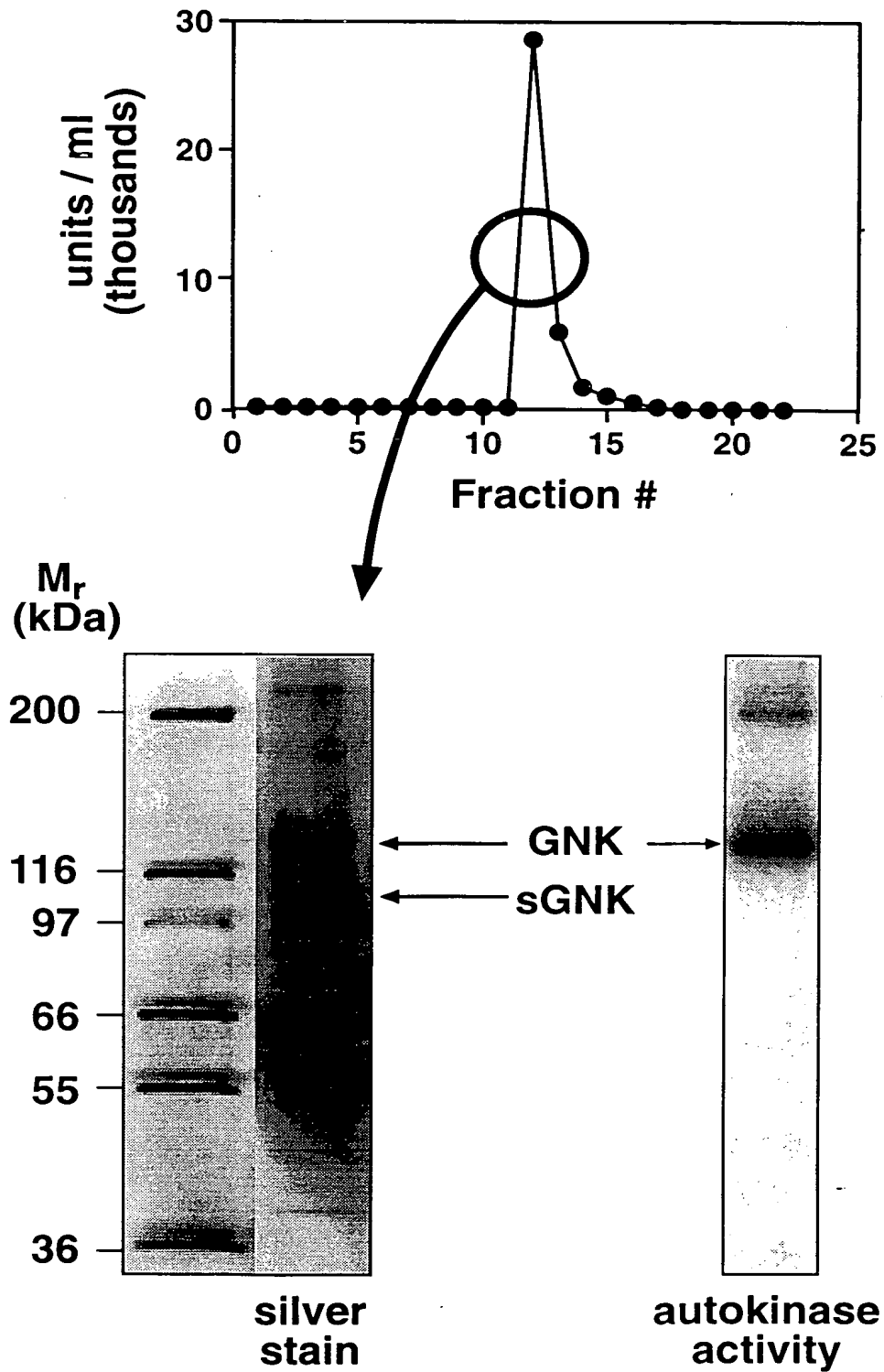


FIGURE 9

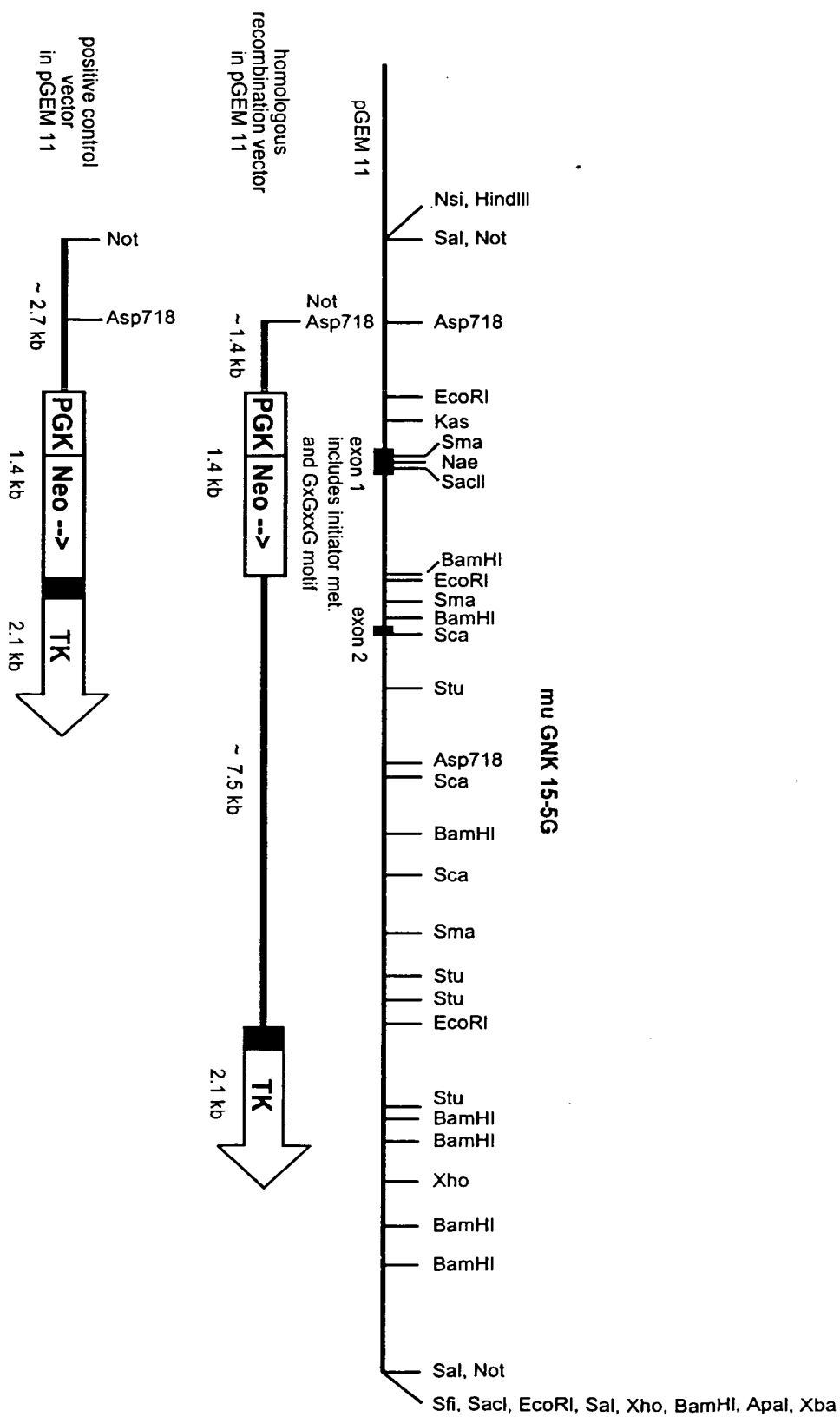


FIGURE 10

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